



SEQUENCE LISTING

Allen, Keith D.
Leviten, Michael W.

<120> TRANSGENIC MICE CONTAINING TRYPTASE GENE
DISRUPTIONS

<130> R-372

<140> US 09/900,754

<141> 2001-07-06

<150> US 60/216,109

<151> 2000-07-06

<150> US 60/223,172

<151> 2000-08-07

<150> US 60/244,111

<151> 2000-10-26

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1122

<212> DNA

<213> Mus musculus

<400> 1

```
atggctctgg ggcccaactg tggcactccta ctgtttctgg ctgtttctgg gtgtggccat 60
ccccagggtt caaactcggg aagtcgaatc gtgggagggc atgctgcccc agcaggcaca 120
tggccgtggc aggctagcct ccgtctgcac aagggtgcacg tgtgtggagg ctccctgctc 180
agtccagaat ggggtgctcac agcagcccac tgcttctctg ggtctgtgaa ctcgctgat 240
tatcagggtc acttgggaga gcttacggtc acactgtctc ccacttctc cactgtaaaa 300
cggatcatca tgtacactgg ctctccagga ccaccggggt ccagtgggga cattgcccctg 360
gtgcagctgt cctccccggg ggccctttcc agccagggtc agcctgtgtg cctcccagag 420
gcctcagctg acttctaccc tgggatgcag tgctgggtga ctggctgggg ctatacaggg 480
gagggagagc ctctgaagcc ccatacaaac cttcaggagg ccaaagtctc tgtggtggat 540
gtaaagacct gcagccaggc ttacaatagt cccaatggca gcctcatcca gccagacatg 600
ctatgcgccc ggggccctgg ggatgcctgc caggatgact ctggagggcc actagtctgc 660
caggtggctg gaacctggca gcaggccggc gtgtgcagct ggggtgaggg ctgtggccgc 720
cctgaccgcc ctggcgtcta tgcccgggtt actgcctatg taaactggat ccaccaccac 780
atccccgaag caggggggctc aggaatgcaa gggcttccct gggctcctct cctggctgcc 840
ctcttctggc caagcctctt cctgctgctg gtctctggag tcctgatggc caagtactgg 900
ctgagctctc cctccacgc ggccctcgga ctctgaatga ggtgtagcaa ccaacccaag 960
tgtctttctt aaataagtta gtgtttattc agtttgcttt gccctcccc tccccttagc 1020
tttgacttag gaagccaaag ttttctgcat cagattattg caacatttaa cctgaatttg 1080
tagaacggat gacataaagc aaatggatgt caaaaaaaaaa aa 1122
```

<210> 2

<211> 311

<212> PRT

<213> Mus musculus

<400> 2

Met Ala Leu Gly Pro Asn Cys Gly Ile Leu Leu Phe Leu Ala Val Ser

1

5

10

15

Gly	Cys	Gly	His	Pro	Gln	Val	Ser	Asn	Ser	Gly	Ser	Arg	Ile	Val	Gly	
			20					25					30			
Gly	His	Ala	Ala	Pro	Ala	Gly	Thr	Trp	Pro	Trp	Gln	Ala	Ser	Leu	Arg	
	35						40				45					
Leu	His	Lys	Val	His	Val	Cys	Gly	Gly	Ser	Leu	Leu	Ser	Pro	Glu	Trp	
	50					55					60					
Val	Leu	Thr	Ala	Ala	His	Cys	Phe	Ser	Gly	Ser	Val	Asn	Ser	Ser	Asp	
65					70					75					80	
Tyr	Gln	Val	His	Leu	Gly	Glu	Leu	Thr	Val	Thr	Leu	Ser	Pro	His	Phe	
			85						90					95		
Ser	Thr	Val	Lys	Arg	Ile	Ile	Met	Tyr	Thr	Gly	Ser	Pro	Gly	Pro	Pro	
			100					105					110			
Gly	Ser	Ser	Gly	Asp	Ile	Ala	Leu	Val	Gln	Leu	Ser	Ser	Pro	Val	Ala	
	115						120					125				
Leu	Ser	Ser	Gln	Val	Gln	Pro	Val	Cys	Leu	Pro	Glu	Ala	Ser	Ala	Asp	
	130					135					140					
Phe	Tyr	Pro	Gly	Met	Gln	Cys	Trp	Val	Thr	Gly	Trp	Gly	Tyr	Thr	Gly	
145					150					155					160	
Glu	Gly	Glu	Pro	Leu	Lys	Pro	Pro	Tyr	Asn	Leu	Gln	Glu	Ala	Lys	Val	
			165						170					175		
Ser	Val	Val	Asp	Val	Lys	Thr	Cys	Ser	Gln	Ala	Tyr	Asn	Ser	Pro	Asn	
			180					185					190			
Gly	Ser	Leu	Ile	Gln	Pro	Asp	Met	Leu	Cys	Ala	Arg	Gly	Pro	Gly	Asp	
	195						200					205				
Ala	Cys	Gln	Asp	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Gln	Val	Ala	Gly	
	210					215					220					
Thr	Trp	Gln	Gln	Ala	Gly	Val	Val	Ser	Trp	Gly	Glu	Gly	Cys	Gly	Arg	
225					230					235					240	
Pro	Asp	Arg	Pro	Gly	Val	Tyr	Ala	Arg	Val	Thr	Ala	Tyr	Val	Asn	Trp	
			245						250					255		
Ile	His	His	His	Ile	Pro	Glu	Ala	Gly	Gly	Ser	Gly	Met	Gln	Gly	Leu	
		260						265					270			
Pro	Trp	Ala	Pro	Leu	Leu	Ala	Ala	Leu	Phe	Trp	Pro	Ser	Leu	Phe	Leu	
	275					280						285				
Leu	Leu	Val	Ser	Gly	Val	Leu	Met	Ala	Lys	Tyr	Trp	Leu	Ser	Ser	Pro	
	290					295					300					
Ser	His	Ala	Ala	Ser	Glu	Leu										
305					310											

<210> 3
 <211> 200
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Targeting Vector

<400> 3
 ggagtcacatgg agggctccca gagaaagggc attgagcaga atgccggtct ccagattccc 60
 tcaccaacag tgtctcctct ggatcagggt gtggccatcc ccaggtttca aactcgggaa 120
 gtcgaatcgt gggagggcat gctgccccag caggcacatg gccgtggcag gctagcctcc 180
 gtctgcacaa ggtgacgtgt 200

<210> 4
 <211> 200
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Targeting Vector

<400> 4

ctccactgta	aaacggatca	tcatgtacac	tggctctcca	ggaccaccgg	ggtccagtgg	60
ggacattgcc	ctggtgcage	tgctctcccc	ggtggccctt	tccagccagg	tccagcctgt	120
gtgcctccca	gaggcctcag	ctgacttcta	ccctgggatg	cagtgcctggg	tgactggctg	180
gggctataca	ggggagggag					200